

Thu Nov 29 08:24:22 2001

us-09-516-052-2_copy_28_177.rsp

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuLink Ltd.

us-09-516-052-2_copy_28_177

us-09-516-052-2_copy_28_177
1 RECDQYMPFIANYRIRIKRIRI... YNYGMUDOSKYNMCCOPYON 150

Perfect score: 804
Sequence: 1 RECDQYMPFIANYRIRIKRIRI... YNYGMUDOSKYNMCCOPYON 150

Scoring table: BLASTSUM62
Gapop 10.0, Gapext 0.5

Search: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: SPTREMBL-16:1
1: sp-archaea:1
2: sp-bacteria:1
3: sp-fungi:1
4: sp-human:1
5: sp-invertebrate:1
6: sp-mammal:1
7: sp-misc:1
8: sp-organole:1
9: sp-phage:1
10: sp-plant:1
11: sp-rodent:1
12: sp-unclassified:1
13: sp-vertebrate:1
14: sp-virus:1

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	804	100.0	208	10	081130 arabidopsis
2	804	100.0	208	10	095868 arabidopsis
3	452.6	56.8	205	10	096310 arabidopsis
4	381	47.4	161	10	023313 arabidopsis
5	381	47.4	187	10	023634 arabidopsis
6	381	47.4	190	10	096313 arabidopsis
7	381	47.4	190	10	096313 arabidopsis
8	381	47.4	190	10	096313 arabidopsis
9	381	47.4	190	10	096313 arabidopsis
10	381	47.4	190	10	096313 arabidopsis
11	381	47.4	190	10	096313 arabidopsis
12	381	47.4	190	10	096313 arabidopsis
13	381	47.4	190	10	096313 arabidopsis
14	381	47.4	190	10	096313 arabidopsis
15	381	47.4	190	10	096313 arabidopsis
16	381	47.4	190	10	096313 arabidopsis
17	381	47.4	190	10	096313 arabidopsis
18	381	47.4	190	10	096313 arabidopsis
19	381	47.4	190	10	096313 arabidopsis

Result No.	Score	Query Match	Length	DB ID	Description
20	276	34.3	403	5	017286 caenorhabditis
21	216	26.9	123	10	091558 arabidopsis
22	166	20.6	162	10	091558 arabidopsis
23	166	20.6	162	10	091558 arabidopsis
24	166	20.6	162	10	091558 arabidopsis
25	166	20.6	162	10	091558 arabidopsis
26	166	20.6	162	10	091558 arabidopsis
27	166	20.6	162	10	091558 arabidopsis
28	166	20.6	162	10	091558 arabidopsis
29	166	20.6	162	10	091558 arabidopsis
30	166	20.6	162	10	091558 arabidopsis
31	166	20.6	162	10	091558 arabidopsis
32	166	20.6	162	10	091558 arabidopsis
33	166	20.6	162	10	091558 arabidopsis
34	166	20.6	162	10	091558 arabidopsis
35	166	20.6	162	10	091558 arabidopsis
36	166	20.6	162	10	091558 arabidopsis
37	166	20.6	162	10	091558 arabidopsis
38	166	20.6	162	10	091558 arabidopsis
39	166	20.6	162	10	091558 arabidopsis
40	166	20.6	162	10	091558 arabidopsis
41	166	20.6	162	10	091558 arabidopsis
42	166	20.6	162	10	091558 arabidopsis
43	166	20.6	162	10	091558 arabidopsis
44	166	20.6	162	10	091558 arabidopsis
45	166	20.6	162	10	091558 arabidopsis

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	804	100.0	208	10	081130 arabidopsis
2	804	100.0	208	10	095868 arabidopsis
3	452.6	56.8	205	10	096310 arabidopsis
4	381	47.4	161	10	023313 arabidopsis
5	381	47.4	187	10	023634 arabidopsis
6	381	47.4	190	10	096313 arabidopsis
7	381	47.4	190	10	096313 arabidopsis
8	381	47.4	190	10	096313 arabidopsis
9	381	47.4	190	10	096313 arabidopsis
10	381	47.4	190	10	096313 arabidopsis
11	381	47.4	190	10	096313 arabidopsis
12	381	47.4	190	10	096313 arabidopsis
13	381	47.4	190	10	096313 arabidopsis
14	381	47.4	190	10	096313 arabidopsis
15	381	47.4	190	10	096313 arabidopsis
16	381	47.4	190	10	096313 arabidopsis
17	381	47.4	190	10	096313 arabidopsis
18	381	47.4	190	10	096313 arabidopsis
19	381	47.4	190	10	096313 arabidopsis

DB	80	INDUILLWAMLLTPEVYVHLKYVLTGVSVSEHRTATNDRGCG	
OY	119	HQPSUGLPPSPVSYXOML166 	
ID	145	GSGSGAP--MYGAGM159	
RESULT	5		
ID	026644	PRELIMINARY: FRT: 187 AA.	
AC	026644:		
D1	01-JAN-1998 (TREMBLEL105, created)		
D1	01-JAN-1998 (TREMBLEL105, last sequence update)		
D1	01-OCT-2000 (TREMBLEL115, last annotation update)		
D1E	TRANS-SCRIPTIION FACTOR (PFAAFMENT).		
GN	HAB4B.		
OS	Arabidopsis thaliana (Monocot cross).		
OC	Eukaryota Viridiplantae Embryophyta Tracheophyta Spermatophyta		
OC	Mangoliophyta eudicotyledons core eudicots Rosidae eucosids II:		
OC	Brassicales Brassicaceae Arabidopsis.		
OX	NCH1:taxid=3702:		
RN	[1]		
RF	SEQUENCE FROM N.A.		
RA	Edwards D., Smith A.G.: Muttay S.A.		
RL	Submitted Aug 1993, 1 kb. Imp175-3000, Trypt. Arabidops		
DL	EMBL: Y13724; CAA74052.1; ..		
DR	Mendel: 26811; Atath12691.26811.		
DK	InterPro: IPR000165; ..		
DK	InterPro: IPR000447; ..		
DR	Pfam: PF00808; CHEF_NFYB_HHRF_1;		
DR	PRINTS: PR00615; CCAATSUBRNA.		
DR	PROSITE: PS03985; CBFA-NFYB_1;		
FT	NONTER 1		
SQ	SEQUENCE: 187 AA: 20255 MW: E4C7A8D9CF37EF40E CPG64:		
Query Match	47.4% Score 611 DB 10 Length 187.		
Post local Similarity	56.6% Prod No. 166 29.		
Matches	74; Conserved loc 28; Mismatches 24; Indels 4; Gaps 12		
OY	1	REDOOYMELAVLPETMPETLSHATITGVAVETIEGVSVITVCANPDGPPEKPT 60	
ID	23	KFLEELLAVSRPFPAFLNNAISGLVSL--MLCVSLSHVLAASPTLTFEEET 12	
OY	61	TATATTWAKSKTEPVNYVETIVEINFELETIDRGSALP QEPDSLEYTGENT 119	
ID	83	INGRDLLWAMTLTFEDVEVLTKVYLCPFFETPCVPDTIGPQGTGGPVPFHQDAVDV 142	
OY	117	CRRGHSHQ 125	
ID	143	CYVGAGAGGR 151	
RESULT	6		
ID	09FCJ3	PRELIMINARY: FRT: 149 AA.	
AC	09FCJ3:		
D1	01-MAR-2001 (TREMBLEL115, created)		
D1	01-MAR-2001 (TREMBLEL115, last sequence update)		
D1	01-MAR-2001 (TREMBLEL115, last annotation update)		
D1E	SIMILARITY TO CYMAT-BOX BINDING TRANSCRIPTION FACTOR.		
GN	Arabidopsis thaliana (Monocot cross).		
OC	Eukaryota Viridiplantae Embryophyta Tracheophyta Spermatophyta		
OC	Mangoliophyta eudicotyledons core eudicots Rosidae eucosids II:		
OC	Brassicales Brassicaceae Arabidopsis.		
OX	NCH1:taxid=3702:		
RN	[1]		
RF	SEQUENCE FROM N.A.		
RA	Krause T., Karch H., Asamiya E., Sato S., Nakamura Y., Kotani H.		
RA	Tabata S.		
RL	"Structural analysis of Arabidopsis thaliana chromosome 5, XI."		
RL	Submitted (Apr-1999) to the EMBL Genbank/Joint databases		

[illegible]


```

Q95119          PRELIMINARY:          PRT:          215 AA.
ID  Q95119
AC  095119
DE  01-MAY-2000 (TEMBLrel. 13, Created)
DI  01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE  01-MAY-2000 (TEMBLrel. 14, Last annotation update)
DE  POTATIVE CCAAT-BOX BINDING TRANSCRIPTION FACTOR.
GN  ATG13570.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC  Magnoliophyta: Eudicotyledones: Core eudicotyledons: Rosidae: eucosids 11:
OC  Brassicales: Brassicaceae: Arabidopsis.
OX  NBI_TaxID:3702.
RN  11
RP  SEQUENCE FROM N.A.
RC  STRAIN=CV. COLUMBIA;
RX  MEDLINE=20083467; PubMed=1661197;
RA  Lin X., Kaul S., Kousley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA  Fujii C.Y., Mason T.M., Bowman G.T., Barnstead M.P., Feldberg T.V.,
RA  Buell C.R., Ketchum K.A., Lee J.L., Rongning C.M., Koo P., Moffat K.S.,
RA  Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon J., Gill J.E.,
RA  Adams M.D., Carrozz A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
RA  Copchaver G.P., Prouss D., Newman W.C., White O., Eisen J.A.,
RA  Salzberg S.L., Fraser C.M., Venter J.C.,
RA  *Sequence and analysis of chromosome 11 of Arabidopsis thaliana.*
RT  Nature 402:761-766(1999).
DR  FMBL: AC007063; AAD2680.1;
DR  HSSP: P48781; 1B67.
DR  InterPro: IPR000166;
DR  InterPro: IPR000947;
DR  Pfam: PF00808; CRED_NFYB_HMF; 1.
DR  PRINTS: PR00615; CCAATSUBNTA.
DR  PROSITE: PS00685; CREA_NFYB; 1.
SQ  SEQUENCE 215 AA: 24619 MW: 9615827972025 CRC64;

Query Match          41.8%; Score 336; DB 10; Length 215.
Best Local Similarity 61.5%; Pred. No. 4,5e-25;
Matches 59; Conservative 24; Mismatches 13; Indels 0; Caps 0;

QY  1 RRDQYMIPIANVIRIMKILPSHAKISDAKFTIQVSVSYISFVTCANPFGQPPPT 60
    ++++++
DB  45 KPDDEPIPIANVIRIMKYPIDNPTKCAKFEVCTVSEELFVTECAATKQLKSKRT 94
    ++++++
DB  61 ITAEDITMAWSKIFPNVDPITVEINRYREIFTR 96
    ++++++
DB  95 INDDITWATITIPFYVAVLKVYDQYDPEDEK 130
    ++++++

RESULT 12
Q00735          PRELIMINARY:          PRT:          186 AA.
ID  Q00735
AC  000735
DE  01-NOV-1996 (TEMBLrel. 01, Created)
DI  01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DE  01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE  POTATIVE COMPONENT OF CCAAT BINDING COMPLEX HAPC.
GN  HAPC.
OS  Emericella nidulans (Aspergillus nidulans).
OC  Fungi: Ascomycota: Pezizomycotina: Eurotiomycetes:
OC  Eurotiales: Trichocomaceae: Emericella.
OX  NBI_TaxID:5072.
RN  11
RP  SEQUENCE FROM N.A.
RC  MEDLINE=95147853; PubMed 7445362;
RA  Mulder N., Scholten J.H., de Boer R.W., Grivell L.A.;
RA  *Sequence of the HAPC transcription factor of Kluyveromyces fragilis
RA  predicts the presence of a novel 4-cysteine zinc-finger motif.*;
RN  Mol. Gen. Genet. 245:96-106(1994).
RN  12
RP  SEQUENCE FROM N.A.
RC  MEDLINE=96285564; PubMed 8709944;
RA  Papadimitrakopoulos F., Andrianopoulos A., Sharp J.A., Davis M.A.,

```

```

RA  Hynes M.J.;
RT  "The hapt gene of Aspergillus nidulans is involved in the expression
RT  of CCAAT-containing promoters.";
RI  Mol. Gen. Genet. 251:412-421(1996).
DR  EMBL: U53441; AAC49411.1;
DR  HSSP: P48781; 1B67.
DR  InterPro: IPR000166;
DR  InterPro: IPR000947;
DR  Pfam: PF00808; CRED_NFYB_HMF; 1.
DR  PRINTS: PR00615; CCAATSUBNTA.
DR  PROSITE: PS00685; CREA_NFYB; 1.
SQ  SEQUENCE 186 AA: 20616 MW: 20CFD50HFBP0BQD CRC64;

```

```

Query Match          41.0%; Score 330; DB 3; Length 186;
Best Local Similarity 50.8%; Pred. No. 1,5e-24;
Matches 63; Conservative 29; Mismatches 26; Indels 8; Caps 2;

QY  1 EFQGYMIPIANVIRIMKILPSHAKISDAKFTIQVSVSYISFVTCANPFGQPPPT 60
    ++++++
DB  42 KQDQWPIPIANVIRIMKILAPENKIAKEKCEVSEISFTISASRCKQDQKRT 101
    ++++++
QY  61 ITAEDITMAWSKIFPNVDPITVEINRYREIFTR 120
    ++++++
DB  102 VNGEDITFAMTSLGFENYVAELKTYLSKYRETSQARQEH-CNRPSS-----SGYACD 153
    ++++++
QY  121 PSKGLP 126
    ++++++
DB  154 PSKGLP 159
    ++++++

RESULT 13
Q73744          PRELIMINARY:          PRT:          206 AA.
ID  Q73744
AC  073744
DE  01-AUG-1998 (TEMBLrel. 07, Created)
DI  01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DE  01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE  NUCLEAR Y/CCAAT BOX BINDING FACTOR K SUBUNIT N-YB.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC  Amphibia: Batrachia: Anura; Mesobatrachia: Pipidae; Pipidae;
OC  Xenopodinae: Xenopus.
OX  NBI_TaxID:8355.
RN  11
RP  SEQUENCE FROM N.A.
RC  Subtilized (JAN-1998) to the FMB/Genbank/EMBL databases.
RA  Herlihy M., Wolfe A.P.;
RA  EMBL: AF041204; AAC82336.1;
DR  HSSP: P48781; 1B67.
DR  InterPro: IPR000166;
DR  InterPro: IPR000947;
DR  Pfam: PF00808; CRED_NFYB_HMF; 1.
DR  PRINTS: PR00615; CCAATSUBNTA.
DR  PROSITE: PS00685; CREA_NFYB; 1.
SQ  SEQUENCE 206 AA: 22582 MW: 95937829AFL41G07 CRC64;

```

```

Query Match          40.9%; Score 328.5; DB 13; Length 206;
Best Local Similarity 53.8%; Pred. No. 2,3e-24;
Matches 63; Conservative 23; Mismatches 24; Indels 7; Caps 1;

QY  1 RRDQYMIPIANVIRIMKILPSHAKISDAKFTIQVSVSYISFVTCANPFGQPPPT 60
    ++++++
DB  52 RRDITLPIANVIRIMKNVAPQTKIAKQKCEVQVSEISFTISASRCKQDQKRT 111
    ++++++
QY  61 ITAEDITMAWSKIFPNVDPITVEINRYREIFTR 117
    ++++++
DB  112 INEDITFAMSGHFSYVPIKTYIKKPF-----AAGCKGIGIVTIDGIG 161
    ++++++

RESULT 14
Q59848

```

